

# SEQUENCE LISTING

<110> Chen, Zhijian J.

<120> A KINASE CAPABLE OF SITE SPECIFIC  
PHOSPHORYLATION OF IκBα

<130> MPI96-031CP1DV1CPACN1M

<140> 10/052005

<141> 2002-01-17

<150> 09/406293

<151> 1999-09-24

<150> 08/825559

<151> 1997-03-19

<150> 08/616499

<151> 1996-03-19

<160> 9

<170> FastSEQ for Windows Version 4.0

<170> PatentIn Release #1.0, Version #1.30

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> Xaa = Leu or Ile

<400> 3

Xaa Tyr Val Glu Xaa Glu Arg  
1 5

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Thr Tyr His Ala Leu Ser Asn Leu Pro Lys  
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<210> 7  
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ccacggtgga  tcagcgcta  cccgagtggt  cgaagtatgc  caaggaagga  agacttcaag  180
aagtcattga  aacccttctc  tctctggaaa  agcagactcg  tactgcttcc  gatatgggat  240
cgacatcccg  tatcttagtt  gcagtagtga  agntgtgcta  tgaggctaaa  gaatgggatt  300
tacttaatta  aaaatattat  tgctttttgt  ccaaaaggcg  gagtcaagtt  aaaaacaagc  360
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ccctgagcaa  cctgccgaaa  gcccgagctg  ccttaacttc  ttctcgaacc  acagcaaattg  180
ccatctactg  cccctctaat  tgcaggccac  cttggacatg  cagtcgggta  ttatccatgc  240
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Arg  Asp  Gly  Leu  Lys  Lys  Glu  Arg  Leu  Leu  Asp  Asp  Arg  His  Asp  Ser
20     25     30
Gly  Leu  Asp  Ser  Met  Lys  Asp  Glu  Glu  Tyr  Glu  Gln  Met  Val  Lys  Glu
35     40     45
Leu  Gln  Glu  Ile  Arg  Leu  Glu  Pro  Gln  Glu  Val  Pro  Arg  Gly  Ser  Glu
50     55     60
Pro  Trp  Lys  Gln  Gln  Leu  Thr  Glu  Asp  Gly  Asp  Ser  Phe  Leu  His  Leu
65     70     75     80
Ala  Ile  Ile  His  Glu  Glu  Lys  Ala  Leu  Thr  Met  Glu  Val  Ile  Arg  Gln
85     90     95
Val  Lys  Gly  Asp  Leu  Ala  Phe  Leu  Asn  Phe  Gln  Asn  Asn  Leu  Gln  Gln
100    105    110
Thr  Pro  Leu  His  Leu  Ala  Val  Ile  Thr  Asn  Gln  Pro  Glu  Ile  Ala  Glu
115    120    125
Ala  Leu  Leu  Gly  Ala  Gly  Cys  Asp  Pro  Glu  Leu  Arg  Asp  Phe  Arg  Gly
130    135    140
Asn  Thr  Pro  Leu  His  Leu  Ala  Cys  Glu  Gln  Gly  Cys  Leu  Ala  Ser  Val
145    150    155    160
Gly  Val  Leu  Thr  Gln  Ser  Cys  Thr  Thr  Pro  His  Leu  His  Ser  Ile  Leu
165    170    175
Lys  Ala  Thr  Asn  Tyr  Asn  Gly  His  Thr  Cys  Leu  His  Leu  Ala  Ser  Ile
180    185    190
His  Gly  Tyr  Leu  Gly  Ile  Val  Glu  Leu  Leu  Val  Ser  Leu  Gly  Ala  Asp
195    200    205
Val  Asn  Ala  Gln  Glu  Pro  Cys  Asn  Gly  Arg  Thr  Ala  Leu  His  Leu  Ala
210    215    220
Val  Asp  Leu  Gln  Asn  Pro  Asp  Leu  Val  Ser  Leu  Leu  Leu  Lys  Cys  Gly
225    230    235    240
Ala  Asp  Val  Asn  Arg  Val  Thr  Tyr  Gln  Gly  Tyr  Ser  Pro  Tyr  Gln  Leu
245    250    255
Thr  Trp  Gly  Arg  Pro  Ser  Thr  Arg  Ile  Gln  Gln  Gln  Leu  Gly  Gln  Leu
260    265    270

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Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser  
 275 280 285  
 Tyr Asp Thr Glu Ser Glu Phe Thr Glu Phe Thr Glu Asp Glu Leu Pro  
 290 295 300  
 Tyr Asp Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu  
 305 310 315